(Rev. 9-27-95)

INTERFERENCE INITIAL MEMORANDUM

Count # 2

BOARD OF PATENT APPEALS AND INTERFERENCES: An interference is found to exist between the following cases:

This interference involves ____ parties

PARTY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY
Yue et al ✓	08/857,217	5-15-97		

If application has been patented, have maintenance fees been paid? ___Yes ___No ___Maintenance fees not due yet

**Accorded the benefit of:

COUNTRY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY

The claim(s) of this party which correspond(s) to this count is(are):

PATENTABLE CLAIMS: 20 — UNPATENTABLE CLAIMS: None

The claim(s) of this party which does(do) not correspond to this count is(are):

PATENTABLE CLAIMS: 2,4-10,19 — UNPATENTABLE CLAIMS: None

PARTY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY
Leungetal ✓	08/842,827	4-17-97		

If application has been patented, have maintenance fees been paid? ___Yes ___No ___Maintenance fees not due yet

**Accorded the benefit of:

COUNTRY	SERIAL NO.	FILING DATE	PATENT NO., IF ANY	ISSUE DATE, IF ANY

The claim(s) of this party which correspond(s) to this count is(are):

PATENTABLE CLAIMS: 2,6,9 — UNPATENTABLE CLAIMS: 5,10-13

The claim(s) of this party which does(do) not correspond to this count is(are):

PATENTABLE CLAIMS: 1,4,14,7-9,15,16 — UNPATENTABLE CLAIMS: 3

Instructions

1. For every patent involved in the interference, check if the fees have been paid by using the **patent number** with the PALM screen CR06.
   If fees are due and they have not been paid, the interference cannot be declared since it would invovlve an expired patent. (35 USC 135(a); 37 CFR 1.606).
2. For each party, separately identify the patentable and unpatentable claims which correspond to the count. (37 CFR 1.601 (f), 1.601 (n), 1.609(b)(2)).
3. For each party, separately identify the patentable and unpatentable claims which do not correspond to the count (37 CFR 1.609(b)(3)).
4. Forward all files including those the benefit of which is being accorded.
5. Keep a copy of the Interference Initial Memorandum and any attachments for your records.

All information requested below must be attached on (a) separate sheet(s) and type-written.

6. On a separate sheet, set forth a single proposed interference count. If any claim of any party is exactly the same word for word as this count, please indicate the party, application or patent number, and the claim number.
7. For each claim designated as corresponding to the count, provide an explanation of why each claim defines the same patentable invention (37 CFR 1.609(b)(2)).
8. For each claim designated as not corresponding to the count, provide an explanation of why each claim defines a separate patentable invention (37 CFR 1.609(b)(3)).
9. For each additional count, if any, repeat steps 2-6 and, additionally, provide an explanation why each count represents a separate patentable invention from every other count (37 CFR 1.609(b)(1)).

DATE	PRIMARY EXAMINER (Signature)	TELEPHONE NO.	ART UNIT
5-13-02	Rebecca Prouty	703-308-4000	1652
DATE	GROUP DIRECTOR SIGNATURE (if required)		
11/6/04	Wood Ward		

**The serial number and filing date of each application the benefit of which is intended to be accorded must be listed. It is not sufficient to merely list the earliest application if there are intervening applications necessary for continuity.

THIS PAGE CAN BE DUPLICATED IF THERE ARE MORE THAN TWO INTERFERING PARTIES.

Count 2:

A isolated polypeptide having the amino acid sequence of SEQ ID NO:1 of 08/857,217 and SEQ ID NO:2 of 08/842,827.

This count is identical to Claim 20 of 08/857,217.

Claims corresponding to the count:

Claim 20 corresponds to the count as it is identical to the count.

Claims not corresponding to the count:

Claims 2, 4-10 and 19 do not correspond to the count as they recite nucleic acids or methods of use thereof which are patentably distinct compounds from the proteins of the count.

The proteins of the count and the nucleic acids of Claims 2, 4-10 and 19 are patentably distinct compounds because they are chemically different, the DNA has other utility besides encoding the proteins such as a hybridization probe and the proteins can be made by another method such as isolation from natural sources or chemical synthesis.

Count 2:

A isolated polypeptide having the amino acid sequence of SEQ ID NO:1 of 08/857,217 and SEQ ID NO:2 of 08/842,827.

This count is identical to Claim 20 of 08/857,217.

Claims corresponding to the count:

Claim 2 corresponds to the count as it recites a Markush group of three human phosphatidic acid phosphatases one of which is the polypeptide of the count. Thus the count would anticipate this claim. However, the claim is broader in scope than the count as it also embraces subject matter which would be non-obvious over the polypeptide of the count which was not disclosed by application 08/857,217. The polypeptides of SEQ ID NOS 4 and 8 of 08/842,827 are distinct and non-obvious over the polypeptide of the count as the disclosure of one human phosphatidic acid phosphatase (such as that of the count) in no way suggests to the ordinary skilled artisan that another structurally different human phosphatidic acid phosphatase of a defined specific structure exists.

Claims 5 and 10-13 corresponds to the count as they recite methods of dephosphorylating a substrate using a human

phosphatidic acid phosphatase which includes the polypeptide of the count.

Kai et al. teach the isolation of porcine PAP, the isolation of and expression of the mouse PAP gene and that PAPs are important enzymes in glycerolipid biosynthesis as well as signal transduction pathways. Therefore, as the polypeptide of the count is a human PAP, it would have been prima facie obvious to recombinantly produce the polypeptide of the count and to use this enzyme for the dephosphorylation of phosphatidic acid and the regulation of signal transduction. However, these claims are not patentable because the scope of the human phosphatidic acid phosphatases which may be used is not limited to the polypeptide of the count (i.e., a specific human phosphatidic acid phosphatase) but include the use of human phosphatidic acid phosphatases suggested by the prior art such as that encoded by the human gene suggested by GENBANK entries AA040858, W04968 or H68363.

Each of GENBANK entries W04968, H68363, and AA040858 disclose a fragment of human cDNA which comprises a sequence highly homologous to a portion of the sequence of the mouse PAP gene disclosed by Kai et al. It is well known in the art that each EST corresponds to the production of some protein as ESTs are fragments of cDNAs which are produced by reverse

transcription from mRNAs of a particular cell type. Only expressed proteins have corresponding mRNAs in a cell and thus each EST corresponds to an expressed protein. While a EST encodes only a portion of the cDNA encoding a particular protein, each EST clearly provides a suggestion that the cell from which the EST was reverse transcribed expressed a corresponding protein. The high homology of the cited ESTs to the mouse PAP gene disclosed by Kai et al. clearly suggests that the protein to which each of these ESTs correspond is the human homolog of the protein of Kai et al. As such it would have been obvious to one of ordinary skill in the art that there is a human homolog of the PAP of Kai et al. which is highly homologous to the mouse and porcine proteins.

Therefore, as Kai et al. teach that type 2 PAPs such as that encoded by the disclosed gene play a role in the regulation of signal transduction by phospholipase D, it would have been obvious to one of ordinary skill in the art to isolate the gene encoding the human homolog of the porcine and mouse PAPs disclosed by Kai et al., to recombinantly express this gene to produce the human PAP and to use this enzyme for the dephosphorylation of phosphatidic acid and the regulation of signal transduction.

Claim 13 is further unpatentable in view of Kai et al. and any one of GENBANK entries AA040858, W04968 or H68363 as discussed above, and further in view of Brindley et al.

Kai et al., AA040858, W04968 and H68363 are discussed above.

Brindley et al. teach that mammalian type 2 PAPs dephosphorylate phosphatidic acid, lysophosphatidic acid, sphingosine-1-phosphate and ceramide-1-phosphate to generate products important in signal transduction pathways.

Therefore, as Kai et al. and Brindley teach that type 2 PAPs such as that encoded by the disclosed gene play a role in the regulation of signal transduction by phospholipase D and other proteins, it would have been obvious to one of ordinary skill in the art to isolate the human homolog of the porcine and mouse PAPs disclosed and to use this enzyme for the dephosphorylation of lysophosphatidic acid, sphingosine-1-phosphate and ceramide-1-phosphate and the regulation of signal transduction.

Claim 6 corresponds to the count as it recites a method of dephosphorylating a substrate using the human phosphatidic acid phosphatase of the count.

Kai et al. teach the isolation of porcine PAP, the isolation of and expression of the mouse PAP gene and that PAPs are important enzymes in glycerolipid biosynthesis as well as signal transduction pathways. Therefore, as the polypeptide of the

count is a human PAP, it would have been prima facie obvious to recombinantly produce the polypeptide of the count and to use this enzyme for the dephosphorylation of phosphatidic acid and the regulation of signal transduction.

Claims not corresponding to the count:

Claims 1, 3, 4, and 14 do not correspond to the count as they recite nucleic acids or methods of use thereof which are patentably distinct compounds from the proteins of the count.

The proteins of the count and the nucleic acids of Claims 1, 3, 4 and 14 are patentably distinct compounds because they are chemically different, the DNA has other utility besides encoding the proteins such as a hybridization probe and the proteins can be made by another method such as isolation from natural sources or chemical synthesis.

Claims 7-9 do not correspond to the count as they recite methods of use of human phosphatidic acid phosphatases different in structure from the human PAP of the count. The disclosure of one human phosphatidic acid phosphatase (such as that of the count) in no way suggests to the ordinary skilled artisan that another structurally different human phosphatidic acid phosphatase of a defined specific structure exists.

Claims 15 and 16 do not correspond to the count as they recite nucleic acids encoding human phosphatidic acid phosphatases or methods of use thereof which encode structurally distinct human phosphatidic acid phosphatases from the human phosphatidic acid phosphatase of the count. The disclosure of one human phosphatidic acid phosphatase (such as that of the count) in no way suggests to the ordinary skilled artisan that a gene encoding another structurally different human phosphatidic acid phosphatase of a defined specific structure exists.